昆 虫 学 报 *Acta Entomologica Sinica*，November 2008，51(11)：1177－1186 ISSN 0454-6296

Diversity of gamasid mites on small mammals in the surrounding areas of Erhai Lake in Yunnan，China

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Abstract: The aim was to study the species diversity，community structure，similarity，distribution and niche of gamasid mites on the body surface of 3 303 small mammals in the surrounding areas of Erhai Lake in Dali，Yunnan by using Shannon-Wiener，hierarchical cluster analysis (SPSS 13.0) and Levins' niche. The investigated site was an important focus of epidemic hemorrhagic fever，where stands alongside three cordilleras surrounding Erhai Lake，namely Eastern Wuliang Mountain，Southern Ailao Mountain and Western Cangshan Mountain. The three confined oriented areas formed different landscapes within the same zone for inartificial barrier's isolation of Erhai Lake. The small mammal hosts were captured from three differently oriented areas belong to 7 families，15 genera and 21 species in 4 orders (Rodentia，Insectivora，Scandentia and Carnivora)，while 23 196 individuals of gamasid mites collected from the body surface of the small mammal hosts are identified into 6 families，16 genera and 43 species. The results reveal that the community structure of gamasid mites is complex with high species diversity. The distribution of gamasid mites and their corresponding hosts are quite uneven in differently orientations，but dominant species beside gamasid mites on the same dominant small mammal host in differently oriented areas beside Erhai Lake are homologous. The results indicate that habitat influences the species composition and distribution of gamasid mites and their corresponding hosts. Gamasid mite communities on their corresponding hosts are similar if the taxonomic position and habitats of the hosts (small mammals) are similar. The abundance and diversity of gamasid mites on small mammals across different sites are determined mainly by host identity and by the habitats where the hosts live. This might be an ecological evidence of co-evolution between small mammals and gamasid mites. But by using the niche breadth of gamasid mites，host-specificity of gamasid mites are low，this may imply that the co-evolution between small mammals and gamasid mites exist，but the degree is not high.

Key words: Acari; gamasid mite; community ecology; co-evolution; different landscapes within the same zone; small mammal; Yunnan

1 INTRODUCTION

Gamasid mites (Acari，Parasitiformes，Mesostigmata) (Deng *et al*.，1993) are a large group of mesostigmatid mites with different ecological behaviors. Some species are free-living mites and others are ectoparasites. The species that parasitize small mammals，especially rodents，are important medical arthropods and some of them have been suspected to be the potential vectors or reservoir hosts of epidemic hemorrhagic fever and some other zoonoses，such as murine typhus，rabbit fever and plague (Chin and Li，1991; Guo *et al*.，1999; Chin，1999; Sasaki *et al*.，2002) as well as the acariasis，which is caused by the direct parasitism of some gamasid mites within the human body and skin anaphylaxis by the mites' biting (Adler and Wills，2003; Durden *et al*.，2004). More than 20 kinds of zoonoses (including plague) have been suspected to be related with gamasid mites (Luo *et al*.，2006). Dali of Yunnan Province is an important focus of epidemic hemorrhagic fever and other mite-borne diseases. Therefore，it is of important medical significance to study species diversity，community structure，similarity，distribution and niche of gamasid mites in Dali of Yunnan Province. Gamasid mites have been regarded as an important category of mite-borne diseases with complicated ecological behavior，therefore ecological research is of great importance in the surveillance and control programme of them. Guo and his colleagues made a great contribution to studying the transmission disease，taxonomy，ecology of mites and

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基金项目：国家自然科学基金项目(30760226)

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收稿日期 Received：2008-05-23；接受日期 Accepted：2008-10-21

described a few new mite species, but few studies were reported on the ecology of gamasid mites in different landscapes in the same zone where the longitude, latitude, altitude and fauna are homologous for inartificial barrier's isolation. This paper is an attempt to illustrate the species diversity, community structure, similarity, niche and distribution of gamasid mites in different landscapes within the same zone, the surrounding areas of Erhai Lake in Dali of Yunnan belonging to Middle Subregion of Hengduan Mountain. The total individuals of mites and small mammals in the Middle Subregion of Hengduan Mountains are the most plentiful in the five geographical subregions (Luo *et al*., 2007). Therefore ecological research is of great importance in the surveillance and control programme of them in the Middle Subregion of Hengduan Mountains. The paper is also an attempt to illustrate the co-evolution between gamasid mites and their hosts from some ecological evidences.

2 MATERIALS AND METHODS

2.1 Investigation sites

An investigation of gamasid mites on the body surface of small mammals was carried out in the areas beside Erhai Lake in Dali, Yunnan from 2003 to 2004, an important focus of epidemic hemorrhagic fever and other mite-borne diseases. A total of 3 303 small mammal hosts were captured from three differently oriented areas which stand alongside three cordilleras surrounding Erhai Lake (a famous fresh water lake in Southwestern China), namely Eastern Wuliang Mountain, Southern Ailao Mountain and Western Cangshan Mountain. The three confined oriented areas formed three different landscapes within the same zone for inartificial barrier's isolation of Erhai Lake. The survey was made in 4 kinds of habitats (indoor habitats, cultivated fields, shrub areas and forest) in each oriented area beside Erhai Lake (99°58′ – 100°27′ E, 25°25′ – 25°58′ N). At 1 950 – 2 050 m above sea level, the average annual temperature is 15.1℃ and the average precipitation is 110 cm.

2.2 Collection and identification

Small mammal hosts were randomly captured with cage-traps (10 cm × 12 cm × 18 cm) baited with apples and oil-fried peanuts. The cage-traps were examined and re-baited each morning. A total of 100 traps were used for each study site. Twenty trap stations were set at 10 m intervals along five trap lines. Trap line were arranged at 10 m intervals. The traps were checked for three consecutive days, and then moved to another place in the same site until the end of observations. A total of 1 500 traps were checked in every site. The trapped small mammals were put into white cloth bags in the field and brought to the laboratory for identification according to their body shape, size and color, and some measurements such as body length, ear length and length of the hind feet. The individuals of the gamasid mites on the body surface of their corresponding small mammal hosts were all collected with fine forceps and preserved in labeled vials containing 70% ethanol until they were identified. Mites were rinsed with clean water several times to remove the alcohol, Hoyer's solution (Deng *et al*., 1993) were used to mount specimens on glass slides for viewing under a stereomicroscope, which were then made transparent in the mixed solution of pure ethanol and xylene (Xylol). After transparent process, the gamasid mite specimens were mounted on slides by using abienic balsam separately. Each individual gamasid mite specimen was finally identified under a microscope after drying process (Guo *et al*., 1999, 2000; Luo *et al*., 2007; Men *et al*., 2007).

2.3 Statistical analysis

The measurement of community structure includes four basic parameters: species richness (S), the diversity index (H'), evenness (J') and dominance index (C'). The diversity index and evenness are based on Shannon-Wiener's method. The four basic parameters of every mite community are calculated as the following formulae (Guo, 1999; Guo *et al*., 2000; Guo, 2004).

$$S = \sum S_i;$$

$$H' = -\sum_{i=1}^{S}(N_i/N)\ln(N_i/N);$$

$$J' = H'/\ln S;$$

$$C' = \sum_{i=1}^{S}(N_i/N)^2$$

Where S_i represents species i in a certain gamasid mite community, N_i and N represent the individuals of gamasid mite species i and the total gamasid mite individuals.

The ectoparasitic gamasid mite species on the body surface of a certain species of small mammal are regarded as a community of mites. On the basis of defining the communities, the constituent ratio (Cr), gamasid mite infected rate (Rm) and gamasid mite index (Im) of the corresponding dominant gamasid mite species on each small mammals species, together with the total gamasid mite infected rate (Rmt) and total gamasid mite index (Imt), are statistically calculated according to the following formulae (Guo *et al*., 2000):

$$Cr = N_i/N;\ Rm = Hm/H;\ Im = M/H;$$

$$Rmt = Hmt/H;\ Imt = Mt/H$$

Here, N_i and N represent the individuals of gamasid mite species i and the total gamasid mite individuals，H stands for the total host individuals，Hm for the individuals of the hosts parasitized by a certain species of gamasid mites，M stands for the individuals of a certain species of gamasid mites，Hmt stands for the total individuals of the hosts parasitized by all the gamasid mites in a certain community，and Mt stands for the total individuals of all the gamasid mites in a certain community.

The similarity of ectoparasitic gamasid mite communities on 19 species of mammals was studied. On the basis of hierarchical cluster analysis，a 19 × 48 primary matrix for the calculation of similarity was formed by 19 community units（19 species of small mammal hosts）and 48 classification variables including 21 dominant gamasid mite constituent ratios（Cr），21 dominant gamasid mite indices（Im），1 total gamasid mite index（Imt），1 total gamasid mite infected rate（Rmt）and 4 community parameters：richness（S），diversity index（H'），evenness（J'）and dominance index（C'）. 19 community units and 48 classification variables form a 19 × 48 primary matrix. The primary matrix is then standardized according to the following formula（Guo *et al.*，1996，2000，2004；Luo *et al.*，2007）：

$$x'_{ab} = (x_{ab} - \bar{x}_b)/\sqrt{\sum (x_{ab} - \bar{x}_b)^2/(n - 1)}$$

$$(a = 1,2,3,\cdots,n;\ b = 1,2,3,\cdots,m),$$

where x_{ab} stands for the bth numerical figure（variable）of the ath case in the primary matrix before the standardization，while x'_{ab} represents the corresponding figures after the standardization. The n and m in the formula represent the number of classification cases and classification variables. On the basis of standardizing the primary matrix，Pearson correlation coefficient（R_{ij}）is used as the similarity measure and then hierarchical cluster analysis is used to compare the similarity between every two classification cases（gamasid mite community units）. In the clustering process，the nearest neighbor cluster method is chosen. The formula of Pearson correlation coefficient（R_{ij}）is shown as follows（Guo *et al.*，1996，1999，2000，2004；Luo *et al.*，2007）：

$$R_{ij} = \frac{\sum_{k=1}^{m}(x_{ik} - \bar{x}_i)(x_{jk} - \bar{x}_j)}{\sqrt{\left[\sum_{k=1}^{m}(x_{ik} - \bar{x}_i)^2\right]\left[\sum_{k=1}^{m}(x_{jk} - \bar{x}_j)^2\right]}}$$

$$\left(\bar{x}_i = (1/m)\sum_{k=1}^{m} x_{ik},\ \bar{x}_j = (1/m)\sum_{k=1}^{m} x_{jk}\right)$$

In the above formulae，R_{ij} stands for the correlation coefficient between ith and jth classification cases（gamasid mite community units）；x_{ik} represents the kth classification variable（index）of ith classification case while x_{jk} the kth classification variable（index）of the jth classification case in the standardized primary matrix；m represents the number of the classification variables（indices）. All the calculation of hierarchical cluster analysis is done with SPSS 13.0 software. The results of the cluster analysis are shown in a dendrogram.

The individuals of each species of gamasid mites on the 19 species of small mammals were calculated into a constituent ratio in the host series，and then Levins' niche breadth was used to determine its host-specificity（Wissinger，1992；Guo *et al.*，1999）. The Levins' niche breadth in this paper has been modified as the following in order to satisfy the actual needs：

$$B_i = \frac{1}{S\sum_{h=1}^{S} P_{ih}^2}$$

Where B_i stands for the niche breadth of gamasid mite species i（species i of gamasid mite），P_{ih} the constituent ratio of gamasid mite species i in the host series h（host species h in the host series），S the total species of small mammals in the host series. A larger value of B_i means a lower host-specieficity of the gamasid mites，and vice versa.

3 RESULTS

3.1 Species diversity and community structure of gamasid mites

Table 1 showed that the species richness（S）of gamasid mites（43）are much greater in number than the species of their hosts（21），most small mammals have two or more species of gamasid mites on their body surface. The diversity index（H'）of most communities of mites were greater than 1，the diversity indices for *Rattus nitidus* and *Apodemus chevrieri* were 138.38 and 2.09，respectively. In addition，evenness（J'），dominance index（C'），the total gamasid mite infected rate（Rmt）and total gamasid mite index（Imt）were also high. The results show that gamasid mites on the body surface of these small mammals is high in species richness，with a high diversity indices，and the community structure of gamasid mites is very diverse.

3.2 Collection and distribution of small mammal hosts and gamasid mites in different landscapes within the same zone

A total of 3 303 individuals of small mammals were captured and identified as 7 families，15 genera and 21 species in 4 orders（Rodentia，Insectivora，Scandentia and Carnivora）. Most small mammal species（19 species）have gamasid mites on their body surface except 2 species of small mammals without gamasid

Table 1 Species diversity and community structure of gamasid mites on small mammals

Small mammal hosts		S	H'	J'	C'	Imt	Rmt（%）
Latin name	Code						
Anourosorex squamipes	1	6	0.1610	0.0899	0.9489	15.4	60.00
Suncus murinus	2	9	1.8735	0.8526	0.2099	0.2833	18.33
Crocidura attenuata	3	6	1.4603	0.8150	0.2707	0.6667	9.09
Berylmys bowersi	4	8	1.1037	0.5308	0.5213	3.667	80.00
Mus musculus	5	1	0	0	1	0.4706	5.88
Mus caroli	6	5	0.8252	0.5127	0.6187	0.9000	50.00
Mus pahari	7	24	0.8935	0.2812	0.5720	14.7143	80.26
Micromys minutus	8	4	1.2425	0.8962	0.3333	0.1500	10.00
Rattus norvegicus	9	16	1.1916	0.4298	0.3635	5.8723	44.08
Rattus nitidus	10	20	138.3809	46.1927	0.4713	37.5020	76.10
Rattus tanezumi	11	6	0.8127	0.4536	0.5764	2.9275	26.94
Rattus steini	12	15	1.5165	0.5600	0.4112	1.580	31.82
Apodemus chevrieri	13	28	2.0853	0.6258	0.2012	0.9774	19.22
Eothenomys miletus	14	24	0.9480	0.3023	0.6702	1.6790	37.23
Niviventer confucianus	15	13	1.2183	0.4750	0.3242	11.56	76.40
Niviventer fulvescens	16	5	1.1211	0.6966	0.3406	24.95	86.36
Dremomys pernyi	17	11	0.4437	0.1850	0.8431	12.1231	61.54
Mustela kathiah	18	2	0.6365	0.9183	0.5556	1.5	50.00
Tupaia belangeri	19	12	1.4299	0.5754	0.3469	0.8934	17.21

Rattus tanezumi = *Rattus flavipectus*；*Rattus steini* = *Rattus rattus sladeni*.

mites. The small mammals without gamasid mites are *Parascaptor leucurus*（Blyth，1850）and *Mus musculus* Linnaeus 1758. The total constituent ratio of 12 dominant small mammal species（with more than 60 individuals for each species）reached 95.46% while the rest 9 species of small mammals reached only 4.54% within the three differently oriented areas. Twenty-one species of small mammals were found in the southern area beside Erhai Lake and the species diversity is the highest of three differently oriented areas. *Eothenomys miletus*，*Apodemus chevrieri*，*Rattus norvegicus* and *Rattus nitidus* were determined as four dominant species of small mammals in the southern area beside Erhai Lake and they accounted for 11.3%，12.90%，16.36% and 19.35% of the total，respectively. However，only 13 species were found in the western area beside Erhai Lake，where the dominant species are *Eothenomys miletus*（15.21%），*Apodemus chevrieri*（21.00%）and *Rattus norvegicus*（19.38%）. In the eastern area beside Erhai Lake 17 small mammal species were found and the dominant species are *Eothenomys miletus*（45.74%），*Apodemus chevrieri*（12.94%），*Mus pahari*（16.43%）and *Rattus norvegicus*（7.51%）（Table 2）.

The 23 196 gamasid mite individuals collected from the body surface of the corresponding small mammal hosts are identified into 6 families，16 genera，43 species. Thirteen species of dominant gamasid mites（more than 100 individuals for each）are the most abundant with 97.69% of the total gamasid mites individuals in all three differently oriented areas，while the remaining 30 gamasid mites species only account for 2.31%（100% − 97.69%）of the total. Forty-two species of gamasid mites were collected from the southern area beside Erhai Lake with the highest species diversity in comparison with the other two differently oriented areas beside Erhai Lake. *Ornithonyssus bacoti*，*Laelaps nuttalli* and *L. guizhouensis* are dominant gamasid mite species from indoor habitats，cultivated fields，shrub areas to forest in the southern area beside Erhai Lake. However，the eastern area beside Erhai Lake had the lower species diversity with only 27 species of gamasid mites collected. *Laelaps echidninus* is dominant gamasid mite species in indoor habitats，while *L. guizhouensis* is the dominant species in other three habitats of the eastern area beside Erhai Lake. In the western area beside Erhai Lake 25 gamasid mite species were found and *Laelaps echidninus* are the dominant gamasid mite species in indoor habitats，while *L. guizhouensis* are the dominant species in other three habitats（Table 2）.

The distribution of gamasid mites and their corresponding hosts are quite uneven in differently oriented areas. The species of small mammals and gamasid mites showed a gradually increasing tendency from indoor habitat，cultivated fields，shrub areas to forest. This may imply that ecological environment influences the species composition and distribution of gamasid mites and their corresponding hosts. Since the investigated sites were choosed in different landscapes in the same zone where the longitude，latitude，altitude and fauna are homologous for inartificial barrier’s isolation， most ecological factors， such as temperature and precipitation have no significant difference in differently oriented， only the influence of habitats variation on distribution of gamasid mites and small mammals. The statistical results showed in three differently oriented areas of Erhai Lake：（1）The main hosts of *L*. *chini* and *L*. *guizhouensis* are *Eothenomys miletus* and *Mus pahari* respecctively；（2）The main host of *L*. *nuttalli* and *L*. *echidninus* are *Rattus norvegicus* and *Rattus nitidus*；（3）The main host of *Eulaelaps dremomydis* is *Dremomy pernyi*；The results of this research revealed that species of gamasid mites on the same host in differently oriented areas are homogeneous and gamasid mite communities on their hosts are similar if the taxonomic position and habitats of the hosts are similar.

Table 2　Distribution of small mammal hosts and gamasid mites in different habitats

Region	Number of species and individuals	Number of species and individuals	Dominant gamasid mite	Dominant host
Eastern area beside Erhai Lake	27（4 502）	17（1 491）	*Laelaps guizhouensis*	*Eothenomys miletus*
Indoor habitats	6（313）	5（178）	*Laelaps echidninus*	*Rattus norvegicus*
Cultivated fields	13（255）	10（223）	*L*. *guizhouensis*	*E*. *miletus*
Shrub areas	14（1434）	12（332）	*L*. *guizhouensis*	*E*. *miletus*
Forest	21（2 500）	10（758）	*L*. *guizhouensis*	*E*. *miletus*
Southern area beside Erhai Lake	42（16 900）	21（1 070）	*Laelaps nuttalli*	*Rattus nitidus*
Indoor habitats	8（2 107）	5（238）	*Ornithonyssus bacoti*	*R*. *norvegicus*
Cultivated fields	17（9 122）	7（228）	*L*. *nuttalli*	*R*. *nitidus*
Shrub areas	28（1 495）	12（181）	*L*. *guizhouensis*	*E*. *miletus*
Forest	34（4 176）	14（423）	*L*. *guizhouensis*	*Tupaia belange*
Western area beside Erhai Lake	25（1 794）	13（742）	*Ornithonyssus bacoti*	*Apodemus chevrieri*
Indoor habitats	11（587）	4（209）	*L*. *echidninus*	*Rattus norvegicus*
Cultivated fields	15（320）	8（200）	*L*. *guizhouensis*	*Eothenomys miletus*
Shrub areas	21（560）	10（228）	*L*. *guizhouensis*	*A*. *chevrieri*
Forest	18（327）	9（105）	*L*. *guizhouensis*	*A*. *chevrieri*

3.3　Similarity comparison of 21 dominant gamasid mites on 19 species small mammals

As defined community， the gamasid mites on 19 species of small mammals form 19 units or classification cases. The primary matrix for calculating community similarity is made of 19 classification cases（19 gamasid community units， unit 1 to 19）and 48 classification indices（variables）. On the basis of the primary matrix and its standardization， the final similarity comparison is carried out in a dendrogram through hierarchical cluster analysis（Fig. 1）. The dendrogram shows that gamasid mite communities on their corresponding hosts are similar if the taxonomic position and habitats of the hosts are similar. For example：（1）the gamasid mite communities on *Niviventer confucianus* and *Niviventer fulvescens* were clustered together in the same group in the dendrogram.（2）The gamasid mite communities on *Rattus norvegicus* and *Rattus tanezumi* are obviously clustered into the same group. However， some gamasid mite communities were not consistent with the taxonomic affinities of their corresponding hosts in the dendrogram. For example， *Mustela kathiah* and *Tupaia belangeri* are not the same family， but merge into the same group； *Berylmys bowersi* and *Mus pahari* are also in the same group； *Suncus murinus* and *Rattus steini* are not the same family， but merge into the same group； *Crocidurina attenuate* and *Apodemus chevrieri* are not the same family， but merge into the same group. The reason for cluster in the latter four groups was that habitats of the hosts are similar. The reason for cluster in the latter four groups was that habitats of the hosts are similar. The results reveal also that similarities of gamasid mite communities are mainly affected by types of the habitats selected by the host mammals.

3.4　Niche breadth and host specificity of gamasid mites

The niche breadth reflects the host-specificity of gamasid mites（the larger the value， the lower the specificity）. The 20 actual niche breadths are arranged in a sequence from smaller to larger values， which reveals the following sequences of the host-specificity of the gamasid mites from high to low： *H*. *glasgowi*， *O*. *bacoti*， *C*. *quadratus*， *H*. *sexsetosus*（Table 3）. Among all the gamasid mites， the host-specificity of *H*. *Sexsetosus*， *H*. *oliviformis* and *H*. *pavlovskii* proves to be the lowest with a wide niche breadth on their hosts， and that of *H*. *glasgowi* and *O*. *bacoti* is the highest with a narrow niche breadth（Table 3）.

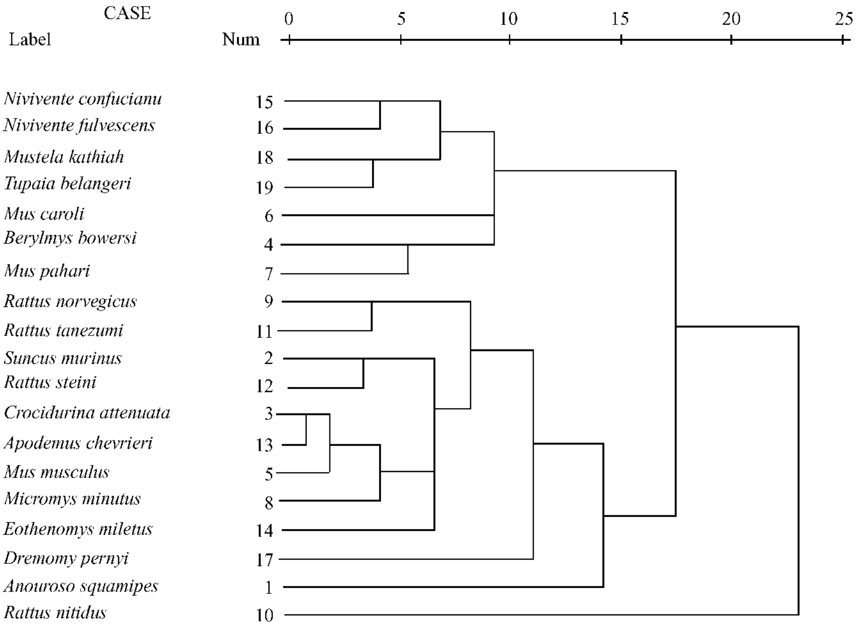

Fig. 1 Hierachical clustering dendrogram of dominant gamasid mite communities on 19 species of small mammal hosts in the surrounding areas of Erhai Lake in Dali, Yunnan

Rattus tanezumi = *Rattus flavipectus*; *Rattus steini* = *Rattus rattus sladeni*.

Table 3 Niche breadths and host-specificity of gamasid mites

Species of gamasid mites	Gamasid mites		Host ranges		Niche breadths	Host-specificity
	Codes	Individuals	Values	Sequences		
Laelaps algericus	1	48	3	3	0.08	6
L. chini	2	1 306	9	8	0.07	5
L. echidninus	3	5 382	12	11	0.09	7
L. liui	4	39	1	1	0.09	7
L. guizhouensis	5	4 232	14	12	0.08	6
L. nuttalli	6	5 923	10	9	0.08	6
L. paucisetosa	7	1 045	4	4	1.44	12
L. traubi	8	571	11	10	0.06	4
L. turkestanicus	9	700	12	11	0.13	8
L. xingyiensis	10	312	3	3	0.19	9
Dipolaelap anourosorecis	11	229	5	5	0.05	3
Eulaelaps dremomydis	12	730	4	4	0.06	4
Hirstionyssus sunci	13	398	11	10	0.08	6
Ornithonyssus bacoti	14	1 688	8	7	0.03	2
Proctolaelaps pygmaeus	15	144	10	9	1.48	13
Androlaelaps singularis	16	38	9	8	0.29	10
Haemolaelaps glasgowi	17	35	2	2	0.01	1
Haemogamasus oliviformis	18	32	5	5	14.01	15
H. sexsetosus	19	49	4	4	55.63	16
Hypoaspis pavlovskii	20	54	9	8	12.51	14

4 CONCLUSION AND DISCUSSION

4.1 The species diversity and community structure of gamasid mites

The abundance and diversity of parasites vary among different populations of host species. In some host-parasite associations, much of the variation seems to depend on the identity of the host species, whereas in other cases it is better explained by local environmental conditions. We captured 3 303 small mammals in the investigated sites and collected 23 196 gamasid mite individuals belonging to 43 species. Guo and his colleagues once investigated 25 counties in Yunnan Province (Guo *et al.*, 2000; Luo *et al.*, 2007) and collected 68 571 gamasid mite individuals from the body surface of 10 803 small mammal hosts, and 112 gamasid mite species were found. Species abundance of gamasid mites is very high, the community diversity indices (Shannon-Wiener′s diversity indices) of gamasid mite on most small mammals are beyond 1. Most small mammals can parasitized more than two species of gamasid mites on their body surface, and the total gamasid mites infected rate (Rmt) are very high. The results suggest that the species diversity of gamasid mites in a certain region or on a certain host is much higher than that of other ectoparasites (sucking lice and fleas). A series of achievements in the fauna researches on ectoparasites have showed that the species of gamasid mites seem to be much more abundant than fleas and sucking lice (Guo *et al*., 2000; Guo *et al*., 2004; Krasnov *et al*., 2008). In 1993, a part of gamasid mites in superfamily Dermanyssoidea was summed up and 232 species of gamasid mites, which belong to 37 genera and 7 families, were recorded in China. If other families in Cohort Gamasina were included, the gamasid mite species in China would be remarkably beyond 232 species (Deng *et al*., 1993). However over 640 flea species belonging to 74 genera and 10 families have been found in China (Wu *et al*., 2007), the species of gamasid mite are much more abundant than fleas. By comparison, the species of fleas are much more abundant than sucking lice. Up to 1999, only 96 species of sucking lice, which belong to 22 genera and 11 families in Order Anoplura, have been recorded in China (Chin, 1999). The results suggest that the species diversity of gamasid mites in a certain region or on a certain host is much higher than that of other ectoparasites (sucking lice and fleas).

4.2 Ecological relationship between gamasid mites and their hosts

The dendrogram shows that gamasid mite communities on their corresponding hosts are similar if the taxonomic position and habitats of the hosts are similar (Fig. 2). For example, the gamasid mite communities on *Niviventer confucianus* and *Niviventer* fulvescens were clustered together in the same group in the dendrogram. The gamasid mite communities on *Rattus norvegicus* and *Rattus tanezumi* are obviously clustered into the same group. The results reveal that some gamasid mite communities on the same genus of small mammal hosts in taxonomy are classified into the same group with a high similarity in hierarchical cluster analysis. When the hosts have a close affinity and habitats of the hosts are similar, the gamasid mite communities on their body surface would tend to be similar with the same or similar dominant gamasid mite species. The results reveal that similarities of gamasid mite communities are affected by the taxonomic position of hosts. This might be an ecological evidence of co-evolution between small mammals and gamasid mite.

However, some gamasid mite communities were not consistent with the taxonomic affinities of their corresponding hosts in the dendrogram. For example, *Mustela kathiah* and *Tupaia belangeri* are not the same family, but merge into the same group for types of the habitats (forests) selected by the host mammals are similar; *Berylmys bowersi* and *Mus pahari* are also not in the same group, but merge into the same group for types of the habitats (forests or shrub areas) selected by the host mammals are similar; *Suncus murinus* and *Rattus steini* are not the same family, but merge into the same group for types of the habitats (cultivated fields or outdoor) selected by the host mammals are similar; *Crocidurina attenuate* and *Apodemus chevrieri* are not the same family, but merge into the same group for types of the habitats (forests, cultivated fields or shrub areas) selected by the host mammals are similar. The results suggest that the types of gamasid mite communities on small mammals are mainly influenced by the habitats in which the hosts live. This suggests that the types of gamasid mite communities on small mammals are influenced not only by their hosts but also by the habitats where the hosts live.

No gamasid mites were collected from 2 species of small mammals. It may result from less sampling numbers since the captured number of *Parascaptor leucurus* (2 individuals) and *Cllosciurus erythrhraeus* (7 individuals) are not enough in the paper, It may be a natural phenomenon that no gamasid mites or few gamasid mites parasitize on the body surface of *Parascaptor leucurus* (2 individuals) and *Cllosciurus erythrhraeus* (7 individuals).

4.3 Distribution of gamasid mites and their corresponding hosts in different landscapes in the same zone

The results of the study revealed that the distribution of gamasid mites and their corresponding hosts in three differently oriented areas beside Erhai Lake is different. More species of gamasid mites and their corresponding small mammal hosts were found in the southern area beside Erhai Lake than in other two differently oriented areas. In addition, a few more dominant gamasid mite species and dominant small mammal hosts were also seen in the southern area beside Erhai Lake than in other two differently oriented areas. The total constituent ratios of hosts, *Eothenomys miletus*, *Apodemus chevrieri*, *Rattus norvegicus* and *Rattus nitidus* were determined as four dominant species of small mammals in the southern area beside Erhai Lake and they accounted for 11.3%, 12.90%, 16.36% and 19.35% of the total respectively, while those of gamasid mites, *Ornithonyssus bacoti*, *Laelaps* *nuttalli* and *Laelaps guizhouensis* are dominant gamasid mites species from indoor habitats, cultivated fields, shrub areas to forest in the southern area beside Erhai Lake with 51.49%, 51.14%, 41.28% and 23.54% of constituent ratios respectively. Therefore these small mammals and gamasid mite species are determined as the main small mammal hosts and gamasid mites.

Table 2 showed that the richness and diversity of small mammals influence the richness and diversity of gamasid mites, the gradient change tendency of community parameters in gamasid mite community was in accordance with those of small mammal community in different habitats. This might be an ecological evidence of co-evolution between small mammals and gamasid mites. Complicated habitats give rise to the high diversity of small mammals and gamasid mites. Adler (1985) suggested that habitat selection is an important determinant factor in small mammal communities. Ecke *et al*.(2002) found that the cover of tall vegetation in the field layer and the structural heterogeneity positively influenced species richness. Most studies showed a positive correlation between habitat heterogeneity, diversity and small mammal species diversity. Our investigation sites were selected in three differently oriented areas beside Erhai Lake. The three regions formed different landscapes in the same zone where the longitude, latitude, altitude and fauna are homologous for inartificial barrier's isolation of Erhai Lake. The southern area beside Erhai Lake is located in the protection areas with a good coverage of ground vegetations, where the abundance and species richness of grasses and shrubs are higher than other two differently oriented areas, and the Ailao Mountain is also biodiversity hotspot. These may influence the distribution of small mammal species. In addition, the boundary effect of transitional fauna or flora may be an important factor of the small mammal distribution. The southern area beside Erhai Lake is the transitional region of Southern Ailao Mountain and Western Cangshan Mountain. The edge effect indicates that the richness and diversity of biology are higher in zoology interleaving zone than contiguous ecosystem. The edge effect may explain that more species of gamasid mites and their corresponding small mammal hosts were found in the southern area beside Erhai Lake than in other two oriented areas. However, the western area beside Erhai Lake also located in the protective areas, species diversity of vegetation is very low in 4 kinds of habitats (indoor habitats, cultivated fields, shrub areas and forest). Numbers of plants are enough in forest but plant species are very singularity in forest, the sort of crop is also singularity, in addition, villager hereabout clean the cough grass in forest annually in their spare time. Human activities decreased the vegetation heterogeneity at the bottom layer of forest. As a result, species diversity of gamasid mites and their corresponding small mammal hosts in the western area beside Erhai Lake is lower than eastern area beside Erhai Lake (non-protective areas). Eastern area beside Erhai Lake belong to non-protection area, Human activities decreased the vegetation heterogeneity at the bottom layer of forest. With forest broken degree deepening, landscape edge effect influence scope and depth also along with it increase, above-ground plant biomass and plant coverage are awfully leanness. But species diversity of vegetation is much higher than the western area beside Erhai Lake in 4 kinds of habitats (indoor habitats, cultivated fields, shrub areas and forest), sorts of crop also are multiplicity and have many orchards in eastern area beside Erhai Lake. The results showed that ecological environment greatly influences the species composition and distribution of gamasid mites and their corresponding small mammal hosts, but species of dominant gamasid mites on the same small mammal host in differently oriented areas are homogeneous.

Distribution of small mammals and gamasid mites varied in different habitats. The species of small mammals and gamasid mites showed a gradually increasing tendency from indoor habitats, cultivated fields, shrub areas to forest. The gradient change of diversity indices of small mammals and gamasid mites in different habitats may be related to the co-evolutionary history between a host and its parasite and environmental conditions.

4.4 Relationship between niche breadth and specificity

A niche breadth could be simply defined as the resource-utilizing scope of a species in a certain community, which has an inverse relationship to the host-specificity of ectoparasites such as fleas, lice, ticks and some mites when the resource-series is formed of hosts (Guo, 1998). The "host range" (the number of host species parasitized by ectoparasites) could reflect the host-specififity to some degree (Guo *et al*., 1993; Guo *et al*., 1999), but it only deals with one side of the specifity (the number of host species) and does not consider the other side, the number of individual ectoparasites like gamasid mites on each species of host. The host range alone is not very effective in evaluating the host-specificity of ectoparasites, in Levins' niche breadth, however, both aspects of the specificity are taken into account. A larger niche breadth means lower host-specificity, the host-specificity further implies that gamasid mites have lowly adapted to the body surface of small mammals.

But by using the niche breadth of gamasid mites，host-specificity of gamasid mites are low，this may imply that the degree of co-evolution between small mammals and gamasid mites is not high．

In conclusion，the paper investigated the species diversity，community structure，similarity，distribution and niche of 23 196 gamasid mites on 3 303 small mammals in the surrounding areas of Erhai Lake．The results showed the species diversity of gamasid mites was higher than sucking lice in comparison with Guo's former reports（Guo *et al*．，2004）．The distribution of gamasid mites and their corresponding hosts are quite uneven in differently oriented areas，but dominant species of gamasid mites on the same dominant small mammal host in differently oriented areas beside Erhai Lake are homologous．This may imply that ecological environment influences the species composition and distribution of gamasid mites and their corresponding hosts．The results of this research reveal also that gamasid mite communities on their corresponding hosts are similar if the taxonomic position and habitats of the hosts are similar．This might be an ecological evidence of co-evolution between small mammals and gamasid mites．But by using the niche breadth of gamasid mites，host-specificity of gamasid mites are low，this may imply that co-evolution between small mammals and gamasid mites exist，but the degree is not high．

The results reveal that the community structure of gamasid mites is complex with high species diversity．The distribution of gamasid mites and their corresponding hosts are quite uneven in differently orientation，but dominant species of gamasid mites on the same dominant small mammal host in differently oriented areas beside Erhai Lake are homologous．The results indicate that habitat influences the species composition and distribution of gamasid mites and their corresponding hosts．Gamasid mite communities on their corresponding hosts are similar if the taxonomic position and habitats of the hosts（small mammals）are similar．The abundance and diversity of gamasid mites on small mammals across different sites are determined mainly by host identity and by the habitats where the hosts live．This might be an ecological evidence of co-evolution between small mammals and gamasid mites．But by using the niche breadth of gamasid mites，host-specificity of gamasid mites are low，this may imply also that the co-evolution between small mammals and gamasid mites exist，but the degree is not high．This suggests that the types of gamasid mite communities on small mammals are influenced not only by their hosts but also by the habitats where the hosts live．

Acknowledgments　We thank some of our colleagues for their help in the field investigation．The project was funded by the Natural Science Foundation of China（Grant No．30760226）．

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中国云南洱海周边小兽体表革螨多样性

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摘要：云南大理洱海周边是我国流行性出血热的流行地区之一。本文目的是运用 Shannon-Wiener、系统聚类分析方法（SPSS 13.0 软件）和 Levins' niche 等对该区 3 303 只小兽体表寄生革螨的物种多样性、群落结构、相似性、分布和生态位进行研究。选择的洱海周边三个不同方位恰好处于东部无量山、南部哀老山和西部苍山，由于洱海的天然隔离使这三个方位形成了同地域异生境的地理景观。在调查点共捕获小兽宿主 3 303 只属 4 目（啮齿目、食虫目、攀鼩目和食肉目）7 科 15 属 21 种，收集到的小兽体表寄生虫革螨 23 196 只被鉴定为 6 科 16 属 43 种。研究结果表明革螨群落结构复杂，物种多样性高。在不同方位革螨和它们相对应宿主的分布是不均匀的，但是洱海周边不同方位同样优势小兽上寄生的优势革螨种是一致的。结果暗示：生境影响着革螨和它们相对应小兽的物种构成和分布，如果小兽宿主的分类地位和生境相似，那么相对应的小兽宿主上的革螨群落就相似；不同方位小兽体表寄生虫革螨的丰富度和物种多样性主要由宿主本身和宿主所栖息的生境决定；这可能是小兽和革螨之间协同进化在生态学上的一个佐证。但通过使用革螨的生态位宽度分析，革螨的宿主特异性很低，这又可能暗示着小兽和革螨之间有协同进化，但协同进化程度不高。

关键词：蜱螨亚纲；革螨；群落生态；协同进化；同地域异生境；小兽；云南

中图分类号：Q968.1　　**文献标识码**：A　　**文章编号**：0454-6296（2008）11-1177-10

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